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In the claims:

1. **(Previously presented)** A method of assigning a sample to a known class, comprising the steps of:
 - a. determining a weighted vote for one or more informative genes for the known class in said sample in accordance with a model built with a weighted voting scheme, wherein the magnitude of each vote depends on the expression level of the one or more informative genes in said sample and on the degree of correlation of the one or more informative genes' expression with class distinction;
 - b. summing the votes to determine a winning class and a prediction strength;
 - c. assigning said sample to the winning class, which winning class is a known class, if the prediction strength is greater than a prediction strength threshold; and
 - d. providing an output indicating assignment of said sample to the winning class, wherein the known class is a cancer disease class selected from any of Acute Lymphoblastic Leukemia (ALL), Acute Myeloid Leukemia (AML), glioblastoma, medulloblastoma, follicular lymphoma, or diffuse large B cell lymphoma.
2. **(Previously presented)** The method of Claim 1, wherein the prediction strength is determined by:
$$(V_{win} - V_{lose}) / (V_{win} + V_{lose}),$$
wherein V_{win} and V_{lose} are the vote totals for one or more winning and losing classes, respectively.
3. **(Original)** The method of Claim 2, wherein the number of informative genes used in the weighted voting scheme is at least 50.
4. **(Previously presented)** The method of Claim 1, wherein the cancer disease class is Acute Lymphoblastic Leukemia (ALL) or Acute Myeloid Leukemia (AML).
5. **(Previously presented)** The method of Claim 2, wherein the cancer disease class is Acute Lymphoblastic Leukemia (ALL) or Acute Myeloid Leukemia (AML).